

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Das, Goutam
- (ii) TITLE OF INVENTION: DNA Molecules for Expression of Polypeptides
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: White & Case
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: United States
 - (F) ZIP: 10036-2787
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/624,398
 - (B) FILING DATE: 04-APR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/SE96/00318
 - (B) FILING DATE: 12-MAR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: SE 9501939-4
 - (B) FILING DATE: 24-MAY-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Thelma A. Chen Cleland
 - (B) REGISTRATION NUMBER: 40,948
 - (C) REFERENCE/DOCKET NUMBER: 1103326-0206
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 319-8200
 - (B) TELEFAX: (212) 354-8113

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: mammary gland

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 82..2319
 (D) OTHER INFORMATION: /product= "bile-salt-stimulated
 lipase"

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 985..1173

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 1174..1377

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 1378..1575

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 1576..2415

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 151..2316

(ix) FEATURE:
 (A) NAME/KEY: polyA_signal
 (B) LOCATION: 2397..2402

(ix) FEATURE:
 (A) NAME/KEY: repeat_region
 (B) LOCATION: 1756..2283

(ix) FEATURE:
 (A) NAME/KEY: 5'UTR
 (B) LOCATION: 1..81

(ix) FEATURE:
 (A) NAME/KEY: repeat_unit
 (B) LOCATION: 1756..1788

(ix) FEATURE:
 (A) NAME/KEY: repeat_unit
 (B) LOCATION: 1789..1821

(ix) FEATURE:
 (A) NAME/KEY: repeat_unit
 (B) LOCATION: 1822..1854

(ix) FEATURE:
 (A) NAME/KEY: repeat_unit
 (B) LOCATION: 1855..1887

- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 1888..1920
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 1921..1953
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 1954..1986
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 1987..2019
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2020..2052
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2053..2085
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2086..2118
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2119..2151
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2152..2184
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2185..2217
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2218..2250
- (ix) FEATURE:
 - (A) NAME/KEY: repeat_unit
 - (B) LOCATION: 2251..2283
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Nilsson, Jeanette
Blackberg, Lars
Carlsson, Peter
Enerback, Sven
Hernell, Olle
Bjursell, Gunnar
 - (B) TITLE: cDNA cloning of human-milk
bile-salt-stimulated lipase and evidence for its
identity to pancreatic carboxylic ester hydrolase
 - (C) JOURNAL: Eur. J. Biochem.
 - (D) VOLUME: 192
 - (F) PAGES: 543-550
 - (G) DATE: Sept.-1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACCTTCTGTA TCAGTTAAGT GTCAAGATGG AAGGAACAGC AGTCTCAAGA TAATGCAAAG	60
AGTTTATTCA TCCAGAGGCT G ATG CTC ACC ATG GGG CGC CTG CAA CTG GTT	111
Met Leu Thr Met Gly Arg Leu Gln Leu Val	
-23 -20 -15	
GTG TTG GGC CTC ACC TGC TGC TGC GCA GTG GCG AGT GGC GCG AAG CTG	159
Val Leu Gly Leu Thr Cys Cys Trp Ala Val Ala Ser Ala Ala Lys Leu	
-10 -5 1	
GGC GCC GTG TAC ACA GAA GGT GGG TTC GTG GAA GGC GTC AAT AAG AAG	207
Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val Asn Lys Lys	
5 10 15	
CTC GGC CTC CTG GGT GAC TCT GTG GAC ATC TTC AAG GGC ATC CCC TTC	255
Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly Ile Pro Phe	
20 25 30 35	
GCA GCT CCC ACC AAG GCC CTG GAA AAT CCT CAG CCA CAT CCT GGC TGG	303
Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His Pro Gly Trp	
40 45 50	
CAA GGG ACC CTG AAG GCC AAG AAC TTC AAG AAG AGA TGC CTG CAG GCC	351
Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala	
55 60 65	
ACC ATC ACC CAG GAC AGC ACC TAC GGG GAT GAA GAC TGC CTG TAC CTC	399
Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu	
70 75 80	
AAC ATT TGG GTG CCC CAG GGC AGG AAG CAA GTC TCC CGG GAC CTG CCC	447
Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg Asp Leu Pro	
85 90 95	
GTT ATG ATC TGG ATC TAT GGA GGC GCC TTC CTC ATG GGG TCC GGC CAT	495
Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly Ser Gly His	
100 105 110 115	
GGG GCC AAC TTC CTC AAC AAC TAC CTG TAT GAC GGC GAG GAG ATC GCC	543
Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala	
120 125 130	
ACA CGC GGA AAC GTC ATC GTG GTC ACC TTC AAC TAC CGT GTC GGC CCC	591
Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg Val Gly Pro	
135 140 145	
CTT GGG TTC CTC AGC ACT GGG GAC GCC AAT CTG CCA GGT AAC TAT GGC	639
Leu Gly Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly	
150 155 160	
CTT CGG GAT CAG CAC ATG GCC ATT GCT TGG GTG AAG AGG AAT ATC GCG	687
Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg Asn Ile Ala	
165 170 175	
GCC TTC GGG GGG GAC CCC AAC AAC ATC ACG CTC TTC GGG GAG TCT GCT	735
Ala Phe Gly Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala	
180 185 190 195	

GGA	GGT	GCC	AGC	GTC	TCT	CTG	CAG	ACC	CTC	TCC	CCC	TAC	AAC	AAG	GGC	783
Gly	Gly	Ala	Ser	Val	Ser	Leu	Gln	Thr	Leu	Ser	Pro	Tyr	Asn	Lys	Gly	
				200					205						210	
CTC	ATC	CGG	CGA	GCC	ATC	AGC	CAG	AGC	GGC	GTG	GCC	CTG	AGT	CCC	TGG	831
Leu	Ile	Arg	Arg	Ala	Ile	Ser	Gln	Ser	Gly	Val	Ala	Leu	Ser	Pro	Trp	
			215					220					225			
GTG	ATC	CAG	AAA	AAC	CCA	CTC	TTC	TGG	GCC	AAA	AAG	GTG	GCT	GAG	AAG	879
Val	Ile	Gln	Lys	Asn	Pro	Leu	Phe	Trp	Ala	Lys	Lys	Val	Ala	Glu	Lys	
		230					235					240				
GTG	GGT	TGC	CCT	GTG	GGT	GAT	GCC	GCC	AGG	ATG	GCC	CAG	TGT	CTG	AAG	927
Val	Gly	Cys	Pro	Val	Gly	Asp	Ala	Ala	Arg	Met	Ala	Gln	Cys	Leu	Lys	
	245					250					255					
GTT	ACT	GAT	CCC	CGA	GCC	CTG	ACG	CTG	GCC	TAT	AAG	GTG	CCG	CTG	GCA	975
Val	Thr	Asp	Pro	Arg	Ala	Leu	Thr	Leu	Ala	Tyr	Lys	Val	Pro	Leu	Ala	
260					265					270					275	
GGG	CTG	GAG	TAC	CCC	ATG	CTG	CAC	TAT	GTG	GGC	TTC	GTG	CCT	GTG	ATT	1023
Gly	Leu	Glu	Tyr	Pro	Met	Leu	His	Tyr	Val	Gly	Phe	Val	Pro	Val	Ile	
				280					285					290		
GAT	GGA	GAC	TTC	ATC	CCC	GCT	GAC	CCG	ATC	AAC	CTG	TAC	GCC	AAC	GCC	1071
Asp	Gly	Asp	Phe	Ile	Pro	Ala	Asp	Pro	Ile	Asn	Leu	Tyr	Ala	Asn	Ala	
			295					300					305			
GCC	GAC	ATC	GAC	TAT	ATA	GCA	GGC	ACC	AAC	AAC	ATG	GAC	GGC	CAC	ATC	1119
Ala	Asp	Ile	Asp	Tyr	Ile	Ala	Gly	Thr	Asn	Asn	Met	Asp	Gly	His	Ile	
		310					315					320				
TTC	GCC	AGC	ATC	GAC	ATG	CCT	GCC	ATC	AAC	AAG	GGC	AAC	AAG	AAA	GTC	1167
Phe	Ala	Ser	Ile	Asp	Met	Pro	Ala	Ile	Asn	Lys	Gly	Asn	Lys	Lys	Val	
	325					330					335					
ACG	GAG	GAG	GAC	TTC	TAC	AAG	CTG	GTC	AGT	GAG	TTC	ACA	ATC	ACC	AAG	1215
Thr	Glu	Glu	Asp	Phe	Tyr	Lys	Leu	Val	Ser	Glu	Phe	Thr	Ile	Thr	Lys	
	340				345					350					355	
GGG	CTC	AGA	GGC	GCC	AAG	ACG	ACC	TTT	GAT	GTC	TAC	ACC	GAG	TCC	TGG	1263
Gly	Leu	Arg	Gly	Ala	Lys	Thr	Thr	Phe	Asp	Val	Tyr	Thr	Glu	Ser	Trp	
			360						365					370		
GCC	CAG	GAC	CCA	TCC	CAG	GAG	AAT	AAG	AAG	AAG	ACT	GTG	GTG	GAC	TTT	1311
Ala	Gln	Asp	Pro	Ser	Gln	Glu	Asn	Lys	Lys	Lys	Thr	Val	Val	Asp	Phe	
			375					380					385			
GAG	ACC	GAT	GTC	CTC	TTC	CTG	GTG	CCC	ACC	GAG	ATT	GCC	CTA	GCC	CAG	1359
Glu	Thr	Asp	Val	Leu	Phe	Leu	Val	Pro	Thr	Glu	Ile	Ala	Leu	Ala	Gln	
		390				395						400				
CAC	AGA	GCC	AAT	GCC	AAG	AGT	GCC	AAG	ACC	TAC	GCC	TAC	CTG	TTT	TCC	1407
His	Arg	Ala	Asn	Ala	Lys	Ser	Ala	Lys	Thr	Tyr	Ala	Tyr	Leu	Phe	Ser	
	405					410					415					
CAT	CCC	TCT	CGG	ATG	CCC	GTC	TAC	CCC	AAA	TGG	GTG	GGG	GCC	GAC	CAT	1455
His	Pro	Ser	Arg	Met	Pro	Val	Tyr	Pro	Lys	Trp	Val	Gly	Ala	Asp	His	
420					425					430					435	

GCA	GAT	GAC	ATT	CAG	TAC	GTT	TTC	GGG	AAG	CCC	TTC	GCC	ACC	CCC	ACG	1503
Ala	Asp	Asp	Ile	Gln	Tyr	Val	Phe	Gly	Lys	Pro	Phe	Ala	Thr	Pro	Thr	
			440						445					450		
GGC	TAC	CGG	CCC	CAA	GAC	AGG	ACA	GTC	TCT	AAG	GCC	ATG	ATC	GCC	TAC	1551
Gly	Tyr	Arg	Pro	Gln	Asp	Arg	Thr	Val	Ser	Lys	Ala	Met	Ile	Ala	Tyr	
			455					460					465			
TGG	ACC	AAC	TTT	GCC	AAA	ACA	GGG	GAC	CCC	AAC	ATG	GGC	GAC	TGG	GCT	1599
Trp	Thr	Asn	Phe	Ala	Lys	Thr	Gly	Asp	Pro	Asn	Met	Gly	Asp	Ser	Ala	
		470					475					480				
GTG	CCC	ACA	CAC	TGG	GAA	CCC	TAC	ACT	ACG	GAA	AAC	AGC	GGC	TAC	CTG	1647
Val	Pro	Thr	His	Trp	Glu	Pro	Tyr	Thr	Thr	Glu	Asn	Ser	Gly	Tyr	Leu	
	485					490					495					
GAG	ATC	ACC	AAG	AAG	ATG	GGC	AGC	AGC	TCC	ATG	AAG	CGG	AGC	CTG	AGA	1695
Glu	Ile	Thr	Lys	Lys	Met	Gly	Ser	Ser	Ser	Met	Lys	Arg	Ser	Leu	Arg	
500					505					510					515	
ACC	AAC	TTC	CTG	CGC	TAC	TGG	ACC	CTC	ACC	TAT	CTG	GGC	CTG	CCC	ACA	1743
Thr	Asn	Phe	Leu	Arg	Tyr	Trp	Thr	Leu	Thr	Tyr	Leu	Ala	Leu	Pro	Thr	
			520					525						530		
GTG	ACC	GAC	CAG	GAG	GCC	ACC	CCT	GTG	CCC	CCC	ACA	GGG	GAC	TCC	GAG	1791
Val	Thr	Asp	Gln	Glu	Ala	Thr	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Glu	
			535					540					545			
GCC	ACT	CCC	GTG	CCC	CCC	ACG	GGT	GAC	TCC	GAG	ACC	GCC	CCC	GTG	CCG	1839
Ala	Thr		Pro	Val	Pro	Thr	Gly	Asp	Ser	Glu	Thr	Ala	Pro	Val	Pro	
		550					555					560				
CCC	ACG	GGT	GAC	TCC	GGG	GCC	CCC	CCC	GTG	CCG	CCC	ACG	GGT	GAC	TCC	1887
Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	
		565				570					575					
GGG	GCC	CCC	CCC	GTG	CCG	CCC	ACG	GGT	GAC	TCC	GGG	GCC	CCC	CCC	GTG	1935
Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	
580					585				590						595	
CCG	CCC	ACG	GGT	GAC	TCC	GGG	GCC	CCC	CCC	GTG	CCG	CCC	ACG	GGT	GAC	1983
Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	
			600					605						610		
TCC	GGG	GCC	CCC	CCC	GTG	CCG	CCC	ACG	GGT	GAC	TCC	GGG	GCC	CCC	CCC	2031
Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	
			615					620					625			
GTG	CCG	CCC	ACG	GGT	GAC	TCC	GGC	GCC	CCC	CCC	GTG	CCG	CCC	ACG	GGT	2079
Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Pro	Pro	Thr	Gly	
		630					635					640				
GAC	GCC	GGG	CCC	CCC	CCC	GTG	CCG	CCC	ACG	GGT	GAC	TCC	GGC	GCC	CCC	2127
Asp	Ala	Gly	Pro	Pro	Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	
	645					650					655					
CCC	GTG	CCG	CCC	ACG	GGT	GAC	TCC	GGG	GCC	CCC	CCC	GTG	ACC	CCC	ACG	2175
Pro	Val	Pro	Pro	Thr	Gly	Asp	Ser	Gly	Ala	Pro	Pro	Val	Thr	Pro	Thr	
660					665					670					675	

GGT GAC TCC GAG ACC GCC CCC GTG CCG CCC ACG GGT GAC TCC GGG GCC	2223
Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala	
680 685 690	
CCC CCT GTG CCC CCC ACG GGT GAC TCT GAG GCT GGC CCT GTG CCC CCC	2271
Pro Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro Val Pro Pro	
695 700 705	
ACA GAT GAC TCC AAG GAA GGT CAG ATG CCT GCA GTC ATT AGG TTT TAA	2319
Thr Asp Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile Arg Phe *	
710 715 720	
CGTCCCATGA GCCTTGGTAT CAAGAGGCCA CAAGAGTGGG ACCCCAGGGG CTCCCCTCCC	2379
ATCTTGAGCT CTTCTGAAT AAAGCCTCAT ACCCCTAAAA AAAAAAAAAA	2428

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Thr Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys	
-23 -20 -15 -10	
Cys Trp Ala Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu	
-5 1 5	
Gly Gly Phe Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp	
10 15 20 25	
Ser Val Asp Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala	
30 35 40	
Leu Glu Asn Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala	
45 50 55	
Lys Asn Phe Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser	
60 65 70	
Thr Tyr Gly Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln	
75 80 85	
Gly Arg Lys Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr	
90 95 100 105	
Gly Gly Ala Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn	
110 115 120	
Asn Tyr Leu Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile	
125 130 135	
Val Val Thr Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr	
140 145 150	

Gly Asp Ala Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met
 155 160 165
 Ala Ile Ala Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro
 170 175 180 185
 Asn Asn Ile Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser
 190 195 200
 Leu Gln Thr Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile
 205 210 215
 Ser Gln Ser Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro
 220 225 230
 Leu Phe Trp Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly
 235 240 245
 Asp Ala Ala Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala
 250 255 260 265
 Leu Thr Leu Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met
 270 275 280
 Leu His Tyr Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro
 285 290 295
 Ala Asp Pro Ile Asn Leu Tyr Ala Asn Ala Ala Asp Ile Asp Tyr Ile
 300 305 310
 Ala Gly Thr Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met
 315 320 325
 Pro Ala Ile Asn Lys Gly Asn Lys Lys Val Thr Glu Glu Asp Phe Tyr
 330 335 340 345
 Lys Leu Val Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys
 350 355 360
 Thr Thr Phe Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln
 365 370 375
 Glu Asn Lys Lys Lys Thr Val Val Asp Phe Glu Thr Asp Val Leu Phe
 380 385 390
 Leu Val Pro Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys
 395 400 405
 Ser Ala Lys Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro
 410 415 420 425
 Val Tyr Pro Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr
 430 435 440
 Val Phe Gly Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp
 445 450 455
 Arg Thr Val Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys
 460 465 470
 Thr Gly Asp Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu
 475 480 485

Pro Tyr Thr Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met
 490 495 500 505
 Gly Ser Ser Ser Met Lys Arg Ser Leu Arg Thr Asn Phe Leu Arg Tyr
 510 515 520
 Trp Thr Leu Thr Tyr Leu Ala Leu Pro Thr Val Thr Asp Gln Glu Ala
 525 530 535
 Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro
 540 545 550
 Thr Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly
 555 560 565
 Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro
 570 575 580 585
 Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser
 590 595 600
 Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val
 605 610 615
 Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp
 620 625 630
 Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Pro
 635 640 645
 Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly
 650 655 660 665
 Asp Ser Gly Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala
 670 675 680
 Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
 685 690 695
 Gly Asp Ser Glu Ala Ala Pro Val Pro Pro Thr Asp Asp Ser Lys Glu
 700 705 710
 Ala Gln Met Pro Ala Val Ile Arg Phe *
 715 720

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Mammary gland

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala	Lys	Leu	Gly	Ala	Val	Tyr	Thr	Glu	Gly	Gly	Phe	Val	Glu	Gly	Val	1	5	10	15
Asn	Lys	Lys	Leu	Gly	Leu	Leu	Gly	Asp	Ser	Val	Asp	Ile	Phe	Lys	Gly	20	25	30	
Ile	Pro	Phe	Ala	Ala	Pro	Thr	Lys	Ala	Leu	Glu	Asn	Pro	Gln	Pro	His	35	40	45	
Pro	Gly	Trp	Gln	Gly	Thr	Leu	Lys	Ala	Lys	Asn	Phe	Lys	Lys	Arg	Cys	50	55	60	
Leu	Gln	Ala	Thr	Ile	Thr	Gln	Asp	Ser	Thr	Tyr	Gly	Asp	Glu	Asp	Cys	65	70	75	80
Leu	Tyr	Leu	Asn	Ile	Trp	Val	Pro	Gln	Gly	Arg	Lys	Gln	Val	Ser	Arg	85	90	95	
Asp	Leu	Pro	Val	Met	Ile	Trp	Ile	Tyr	Gly	Gly	Ala	Phe	Leu	Met	Gly	100	105	110	
Ser	Gly	His	Gly	Ala	Asn	Phe	Leu	Asn	Asn	Tyr	Leu	Tyr	Asp	Gly	Glu	115	120	125	
Glu	Ile	Ala	Thr	Arg	Gly	Asn	Val	Ile	Val	Val	Thr	Phe	Asn	Tyr	Arg	130	135	140	
Val	Gly	Pro	Leu	Gly	Phe	Leu	Ser	Thr	Gly	Asp	Ala	Asn	Leu	Pro	Gly	145	150	155	160
Asn	Tyr	Gly	Leu	Arg	Asp	Gln	His	Met	Ala	Ile	Ala	Trp	Val	Lys	Arg	165	170	175	
Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	Pro	Asn	Asn	Ile	Thr	Leu	Phe	Gly	180	185	190	
Glu	Ser	Ala	Gly	Gly	Ala	Ser	Val	Ser	Leu	Gln	Thr	Leu	Ser	Pro	Tyr	195	200	205	
Asn	Lys	Gly	Leu	Ile	Arg	Arg	Ala	Ile	Ser	Gln	Ser	Gly	Val	Ala	Leu	210	215	220	
Ser	Pro	Trp	Val	Ile	Gln	Lys	Asn	Pro	Leu	Phe	Trp	Ala	Lys	Lys	Val	225	230	235	240
Ala	Glu	Lys	Val	Gly	Cys	Pro	Val	Gly	Asp	Ala	Ala	Arg	Met	Ala	Gln	245	250	255	
Cys	Leu	Lys	Val	Thr	Asp	Pro	Arg	Ala	Leu	Thr	Leu	Ala	Tyr	Lys	Val	260	265	270	
Pro	Leu	Ala	Gly	Leu	Glu	Tyr	Pro	Met	Leu	His	Tyr	Val	Gly	Phe	Val	275	280	285	
Pro	Val	Ile	Asp	Gly	Asp	Phe	Ile	Pro	Ala	Asp	Pro	Ile	Asn	Leu	Tyr	290	295	300	
Ala	Asn	Ala	Ala	Asp	Ile	Asp	Tyr	Ile	Ala	Gly	Thr	Asn	Asn	Met	Asp	305	310	315	320

Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn
 325 330 335
 Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr
 340 345 350
 Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr
 355 360 365
 Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val
 370 375 380
 Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala
 385 390 395 400
 Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr
 405 410 415
 Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly
 420 425 430
 Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala
 435 440 445
 Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met
 450 455 460
 Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly
 465 470 475 480
 Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser
 485 490 495
 Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg
 500 505 510
 Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala
 515 520 525
 Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val Pro Pro Thr Gly
 530 535 540
 Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp Ser Glu Thr Ala
 545 550 555 560
 Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
 565 570 575
 Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala
 580 585 590
 Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro
 595 600 605
 Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly
 610 615 620
 Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro
 625 630 635 640
 Pro Thr Gly Asp Ala Gly Pro Pro Pro Val Pro Pro Thr Gly Asp Ser
 645 650 655

Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val
 660 665 670

Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp
 675 680 685

Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Glu Ala Ala Pro
 690 695 700

Val Pro Pro Thr Asp Asp Ser Lys Glu Ala Gln Met Pro Ala Val Ile
 705 710 715 720

Arg Phe

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Mammary gland

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: /label= Variant_C

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Hansson, Lennart
 Blackberg, Lars
 Edlund, Michael
 Lundberg, Lennart
 Stromqvist, Mats
 Hernell, Olle
- (B) TITLE: Recombinant Human Milk Bile Salt-stimulated
 Lipase
- (C) JOURNAL: J. Biol. Chem.
- (D) VOLUME: 268
- (E) ISSUE: 35
- (F) PAGES: 26692-26698
- (G) DATE: Dec. 15-1993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe Val Glu Gly Val
 1 5 10 15

Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp Ile Phe Lys Gly
 20 25 30

Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn Pro Gln Pro His
 35 40 45

Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe Lys Lys Arg Cys
 50 55 60
 Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly Asp Glu Asp Cys
 65 70 75 80
 Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys Gln Val Ser Arg
 85 90 95
 Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala Phe Leu Met Gly
 100 105 110
 Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu Tyr Asp Gly Glu
 115 120 125
 Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr Phe Asn Tyr Arg
 130 135 140
 Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala Asn Leu Pro Gly
 145 150 155 160
 Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala Trp Val Lys Arg
 165 170 175
 Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile Thr Leu Phe Gly
 180 185 190
 Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr Leu Ser Pro Tyr
 195 200 205
 Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser Gly Val Ala Leu
 210 215 220
 Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp Ala Lys Lys Val
 225 230 235 240
 Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala Arg Met Ala Gln
 245 250 255
 Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu Ala Tyr Lys Val
 260 265 270
 Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr Val Gly Phe Val
 275 280 285
 Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro Ile Asn Leu Tyr
 290 295 300
 Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr Asn Asn Met Asp
 305 310 315 320
 Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile Asn Lys Gly Asn
 325 330 335
 Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val Ser Glu Phe Thr
 340 345 350
 Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe Asp Val Tyr Thr
 355 360 365
 Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys Lys Lys Thr Val
 370 375 380

Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro Thr Glu Ile Ala
 385 390 395 400
 Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys Thr Tyr Ala Tyr
 405 410 415
 Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro Lys Trp Val Gly
 420 425 430
 Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly Lys Pro Phe Ala
 435 440 445
 Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val Ser Lys Ala Met
 450 455 460
 Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Met Gly
 465 470 475 480
 Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr Thr Glu Asn Ser
 485 490 495
 Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser Ser Met Lys Arg
 500 505 510
 Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu Thr Tyr Leu Ala
 515 520 525
 Leu Pro Thr Val Thr Asp Gln Gly Ala Pro Pro Val Pro Pro Thr Gly
 530 535 540
 Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Lys Glu Ala
 545 550 555 560
 Gln Met Pro Ala Val Ile Arg Phe
 565